


## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- 
- (i) APPLICANT: Ruvkun, Gary  
Morris, Jason  
Tissenbaum, Heidi
- (ii) TITLE OF THE INVENTION: AGE-1 POLYPEPTIDES AND RELATED  
MOLECULES AND METHODS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Clark & Elbing LLP  
(B) STREET: 176 Federal Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US97/13914  
(B) FILING DATE: 07-AUG-1997  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/023,382  
(B) FILING DATE: 07-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Elbing, Karen L  
(B) REGISTRATION NUMBER: 35,238  
(C) REFERENCE/DOCKET NUMBER: 08472/704WO2
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617-428-0200  
(B) TELEFAX: 617-428-7045  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	His	Val	Asn	Ile	Leu	His	Pro	Gln	Leu	Gln	Thr	Met	Val	Glu	Gln
1				5					10					15	
Trp	Gln	Met	Arg	Glu	Arg	Pro	Ser	Leu	Glu	Thr	Glu	Asn	Gly	Lys	Gly
			20					25					30		
Ser	Leu	Leu	Leu	Glu	Asn	Glu	Gly	Val	Ala	Asp	Ile	Ile	Thr	Met	Cys
			35					40					45		
Pro	Phe	Gly	Glu	Val	Ile	Ser	Val	Val	Phe	Pro	Trp	Phe	Leu	Ala	Asn
	50					55					60				
Val	Arg	Thr	Ser	Leu	Glu	Ile	Lys	Leu	Ser	Asp	Phe	Lys	His	Gln	Leu
65					70					75				80	
Phe	Glu	Leu	Ile	Ala	Pro	Met	Lys	Trp	Gly	Thr	Tyr	Ser	Val	Lys	Pro
			85						90					95	
Gln	Asp	Tyr	Val	Phe	Arg	Gln	Leu	Asn	Asn	Phe	Gly	Glu	Ile	Glu	Val
			100					105					110		
Ile	Phe	Asn	Asp	Asp	Gln	Pro	Leu	Ser	Lys	Leu	Glu	Leu	His	Gly	Thr
		115					120						125		
Phe	Pro	Met	Leu	Phe	Leu	Tyr	Gln	Pro	Asp	Gly	Ile	Asn	Arg	Asp	Lys
	130					135					140				
Glu	Leu	Met	Ser	Asp	Ile	Ser	His	Cys	Leu	Gly	Tyr	Ser	Leu	Asp	Lys
145					150					155				160	
Leu	Glu	Glu	Ser	Leu	Asp	Glu	Glu	Leu	Arg	Gln	Phe	Arg	Ala	Ser	Leu
			165						170					175	
Trp	Ala	Arg	Thr	Lys	Lys	Thr	Cys	Leu	Thr	Arg	Gly	Leu	Glu	Gly	Thr
		180					185						190		
Ser	His	Tyr	Ala	Phe	Pro	Glu	Glu	Gln	Tyr	Leu	Cys	Val	Gly	Glu	Ser
		195					200					205			
Cys	Pro	Lys	Asp	Leu	Glu	Ser	Lys	Val	Lys	Ala	Ala	Lys	Leu	Ser	Tyr
	210					215					220				
Gln	Met	Phe	Trp	Arg	Lys	Arg	Lys	Ala	Glu	Ile	Asn	Gly	Val	Cys	Glu
225				230						235				240	
Lys	Met	Met	Lys	Ile	Gln	Ile	Glu	Phe	Asn	Pro	Asn	Glu	Thr	Pro	Lys
			245						250					255	
Ser	Leu	Leu	His	Thr	Phe	Leu	Tyr	Glu	Met	Arg	Lys	Leu	Asp	Val	Tyr
		260						265					270		
Asp	Thr	Asp	Asp	Pro	Ala	Asp	Glu	Gly	Trp	Phe	Leu	Gln	Leu	Ala	Gly
	275						280					285			
Arg	Thr	Thr	Phe	Val	Thr	Asn	Pro	Asp	Val	Lys	Leu	Thr	Ser	Tyr	Asp
	290					295					300				
Gly	Val	Arg	Ser	Glu	Leu	Glu	Ser	Tyr	Arg	Cys	Pro	Gly	Phe	Val	Val

305					310					315					320
Arg	Arg	Gln	Ser	Leu	Val	Leu	Lys	Asp	Tyr	Cys	Arg	Pro	Lys	Pro	Leu
				325					330					335	
Tyr	Glu	Pro	His	Tyr	Val	Arg	Ala	His	Glu	Arg	Lys	Leu	Ala	Leu	Asp
			340					345					350		
Val	Leu	Ser	Val	Ser	Ile	Asp	Ser	Thr	Pro	Lys	Gln	Ser	Lys	Asn	Ser
		355				360						365			
Asp	Met	Val	Met	Thr	Asp	Phe	Arg	Pro	Thr	Ala	Ser	Leu	Lys	Gln	Val
	370				375				380						
Ser	Leu	Trp	Asp	Leu	Asp	Ala	Asn	Leu	Met	Ile	Arg	Pro	Val	Asn	Ile
385				390					395					400	
Ser	Gly	Phe	Asp	Phe	Pro	Ala	Asp	Val	Asp	Met	Tyr	Val	Arg	Ile	Glu
			405					410					415		
Phe	Ser	Val	Tyr	Val	Gly	Thr	Leu	Thr	Leu	Ala	Ser	Lys	Ser	Thr	Thr
		420				425					430				
Lys	Val	Asn	Ala	Gln	Phe	Ala	Lys	Trp	Asn	Lys	Glu	Met	Tyr	Thr	Phe
	435					440				445					
Asp	Leu	Tyr	Met	Lys	Asp	Met	Pro	Pro	Ser	Ala	Val	Leu	Ser	Ile	Arg
	450				455				460						
Val	Leu	Tyr	Gly	Lys	Val	Lys	Leu	Lys	Ser	Glu	Glu	Phe	Glu	Val	Gly
465				470					475					480	
Trp	Val	Asn	Met	Ser	Leu	Thr	Asp	Trp	Arg	Asp	Glu	Leu	Arg	Gln	Gly
			485					490					495		
Gln	Phe	Leu	Phe	His	Leu	Trp	Ala	Pro	Glu	Pro	Thr	Ala	Asn	Arg	Ser
		500					505					510			
Arg	Ile	Gly	Glu	Asn	Gly	Ala	Arg	Ile	Gly	Thr	Asn	Ala	Ala	Val	Thr
	515				520						525				
Ile	Glu	Ile	Ser	Ser	Tyr	Gly	Gly	Arg	Val	Arg	Met	Pro	Ser	Gln	Gly
	530				535				540						
Gln	Tyr	Thr	Tyr	Leu	Val	Lys	His	Arg	Ser	Thr	Trp	Thr	Glu	Thr	Leu
545				550					555					560	
Asn	Ile	Met	Gly	Asp	Asp	Tyr	Glu	Ser	Cys	Ile	Arg	Asp	Pro	Gly	Tyr
			565					570					575		
Lys	Lys	Leu	Gln	Met	Leu	Val	Lys	Lys	His	Glu	Ser	Gly	Ile	Val	Leu
		580					585					590			
Glu	Glu	Asp	Glu	Gln	Arg	His	Val	Trp	Met	Trp	Arg	Arg	Tyr	Ile	Gln
		595				600					605				
Lys	Gln	Glu	Pro	Asp	Leu	Leu	Ile	Val	Leu	Ser	Glu	Leu	Ala	Phe	Val
	610				615				620						
Trp	Thr	Asp	Arg	Glu	Asn	Phe	Ser	Glu	Leu	Tyr	Val	Met	Leu	Glu	Lys
625				630					635					640	
Trp	Lys	Pro	Pro	Ser	Val	Ala	Ala	Ala	Leu	Thr	Leu	Leu	Gly	Lys	Arg
			645					650					655		
Cys	Thr	Asp	Arg	Val	Ile	Arg	Lys	Phe	Ala	Val	Glu	Lys	Leu	Asn	Glu
		660					665					670			
Gln	Leu	Ser	Pro	Val	Thr	Phe	His	Leu	Phe	Ile	Leu	Pro	Leu	Ile	Gln
	675					680					685				
Ala	Leu	Lys	Tyr	Glu	Pro	Arg	Ala	Gln	Ser	Glu	Val	Gly	Met	Met	Leu
	690				695					700					
Leu	Thr	Arg	Ala	Leu	Cys	Asp	Tyr	Arg	Ile	Gly	His	Arg	Leu	Phe	Trp
705				710					715					720	

Leu	Leu	Arg	Ala	Glu	Ile	Ala	Arg	Leu	Arg	Asp	Cys	Asp	Leu	Lys	Ser		
				725					730					735			
Glu	Glu	Tyr	Arg	Arg	Ile	Ser	Leu	Leu	Met	Glu	Ala	Tyr	Leu	Arg	Gly		
			740					745					750				
Asn	Glu	Glu	His	Ile	Lys	Ile	Ile	Thr	Arg	Gln	Val	Asp	Met	Val	Asp		
		755				760						765					
Glu	Leu	Thr	Arg	Ile	Ser	Thr	Leu	Val	Lys	Gly	Met	Pro	Lys	Asp	Val		
	770					775					780						
Ala	Thr	Met	Lys	Leu	Arg	Asp	Glu	Leu	Arg	Ser	Ile	Ser	His	Lys	Met		
785					790					795					800		
Glu	Asn	Met	Asp	Ser	Pro	Leu	Asp	Pro	Val	Tyr	Lys	Leu	Gly	Glu	Met		
			805					810						815			
Ile	Ile	Asp	Lys	Ala	Ile	Val	Leu	Gly	Ser	Ala	Lys	Arg	Pro	Leu	Met		
			820					825					830				
Leu	His	Trp	Lys	Asn	Lys	Asn	Pro	Lys	Ser	Asp	Leu	His	Leu	Pro	Phe		
		835					840					845					
Cys	Ala	Met	Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu		
	850					855				860							
Val	Leu	Gln	Val	Leu	Glu	Val	Met	Asp	Asn	Ile	Trp	Lys	Ala	Ala	Asn		
865					870					875					880		
Ile	Asp	Cys	Cys	Leu	Asn	Pro	Tyr	Ala	Val	Leu	Pro	Met	Gly	Glu	Met		
			885					890						895			
Ile	Gly	Ile	Ile	Glu	Val	Val	Pro	Asn	Cys	Lys	Thr	Ile	Phe	Glu	Ile		
			900					905					910				
Gln	Val	Gly	Thr	Gly	Phe	Met	Asn	Thr	Ala	Val	Arg	Ser	Ile	Asp	Pro		
		915					920						925				
Ser	Phe	Met	Asn	Lys	Trp	Ile	Arg	Lys	Gln	Cys	Gly	Ile	Glu	Asp	Glu		
	930					935					940						
Lys	Lys	Lys	Ser	Lys	Lys	Asp	Ser	Thr	Lys	Asn	Pro	Ile	Glu	Lys	Lys		
945					950					955					960		
Ile	Asp	Asn	Thr	Gln	Ala	Met	Lys	Lys	Tyr	Phe	Glu	Ser	Val	Asp	Arg		
			965					970						975			
Phe	Leu	Tyr	Ser	Cys	Val	Gly	Tyr	Ser	Val	Ala	Thr	Tyr	Ile	Met	Gly		
		980						985					990				
Ile	Lys	Asp	Arg	His	Ser	Asp	Asn	Leu	Met	Leu	Thr	Glu	Asp	Gly	Lys		
		995					1000					1005					
Tyr	Val	His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	His	Gly	Lys	Thr	Lys		
	1010					1015					1020						
Leu	Gly	Ile	Gln	Arg	Asp	Arg	Gln	Pro	Phe	Ile	Leu	Thr	Glu	His	Phe		
025				1030						1035					1040		
Met	Thr	Val	Ile	Arg	Ser	Gly	Lys	Ser	Val	Asp	Gly	Asn	Ser	His	Glu		
			1045					1050						1055			
Leu	Gln	Lys	Phe	Lys	Thr	Leu	Cys	Val	Glu	Ala	Tyr	Glu	Val	Met	Trp		
		1060						1065					1070				
Asn	Asn	Arg	Asp	Leu	Phe	Val	Ser	Leu	Phe	Thr	Leu	Met	Leu	Gly	Met		
		1075					1080					1085					
Glu	Leu	Pro	Glu	Leu	Ser	Thr	Lys	Ala	Asp	Leu	Asp	His	Leu	Lys	Lys		
	1090					1095					1100						
Thr	Leu	Phe	Cys	Asn	Gly	Glu	Ser	Lys	Glu	Glu	Ala	Arg	Lys	Phe	Phe		
105				1110					1115					1120			
Ala	Gly	Ile	Tyr	Glu	Glu	Ala	Phe	Asn	Gly	Ser	Trp	Ser	Thr	Lys	Thr		

1125 1130 1135  
 Asn Trp Leu Phe His Ala Val Lys His Tyr  
 1140 1145

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGGAAGCCAT	GGAGCTCGAG	ATCTGATTGC	TGGACACGGA	CGGAACTCCG	ACGTATCTCG	60
CAGATGCATG	TTAACATTTT	ACATCCACAA	CTGCAAACGA	TGGTCGAGCA	GTGGCAAATG	120
CGAGAACGCC	CATCGCTGGA	GACCGAGAAT	GGCAAAGGAT	CGCTGCTCCT	GGAAAATGAA	180
GGTGTGCGAG	ATATCATCAC	TATGTGTCCA	TTCGGAGAAG	TTATTAGTGT	AGTATTTCCG	240
TGGTTTCTTG	CAAATGTGCG	AACATCGCTA	GAAATCAAGC	TATCAGATTT	CAAACATCAA	300
CTTTTCGAAT	TGATTGCTCC	GATGAAGTGG	GGAACATATT	CCGTAAAGCC	ACAGGATTAT	360
GTGTTTCAGAC	AGTTGAATAA	TTTCGGCGAA	ATTGAAGTTA	TATTTAACGA	CGATCAACCC	420
CTGTGCAAAAT	TAGAGCTCCA	CGGCACCTTC	CCAATGCTTT	TTCTCTACCA	ACCTGATGGA	480
ATAAACAGGG	ATAAAGAATT	AATGAGTGAT	ATAAGTCATT	GTCTAGGATA	CTCACTGGAT	540
AAACTGGAAG	AGAGCCTCGA	TGAGGAACTC	CGTCAATTTT	GTGCTTCTCT	CTGGGCTCGT	600
ACGAAGAAAA	CGTGCTTGAC	ACGTGGACTT	GAGGGTACCA	GTCACTACGC	GTTCCCCGAA	660
GAACAGTACT	TGTGTGTTGG	TGAATCGTGC	CCGAAAGATT	TGGAATCAAA	AGTCAAGGCT	720
GCCAAGCTGA	GTTATCAGAT	GTTTTGGAGA	AAACGTAAAG	CGGAAATCAA	TGGAGTTTGC	780
GAGAAAATGA	TGAAGATTCA	AATTGAATTC	AATCCGAACG	AAACTCCGAA	ATCTCTGCTT	840
CACACGTTTC	TCTACGAAAT	GCGAAAATTG	GATGTATACG	ATACCGATGA	TCCTGCAGAT	900
GAAGGATGGT	TTCTTCAATT	GGCTGGACGT	ACCACGTTTG	TTACAAATCC	AGATGTCAAA	960
CTTACGTCTT	ATGATGGTGT	CCGTTTCGGAA	CTGGAAAGCT	ATCGATGCCC	TGGATTTCGTT	1020
GTTTCGCCGAC	AATCACTAGT	CCTCAAAGAC	TATTGTTCGCC	CAAAACCACT	CTACGAACCA	1080
CATTATGTGA	GAGCACACGA	ACGAAAACCT	GCTCTAGACG	TGCTCAGCGT	GTCTATAGAT	1140
AGCACACCAA	AACAGAGCAA	GAACAGTGAC	ATGGTTATGA	CTGATTTTTCG	TCCGACAGCT	1200
TCACTCAAAC	AAGTTTCACT	TTGGGACCTT	GACGCGAATC	TTATGATACG	GCCTGTGAAT	1260
ATTTCTGGAT	TCGATTTCCC	GGCCGACGTG	GATATGTACG	TTCGAATCGA	ATTCAAGTGA	1320
TATGTGGGGA	CACTGACGCT	GGCATCAAAA	TCTACAACAA	AAGTGAATGC	TCAATTTGCA	1380
AAATGGAATA	AGGAAATGTA	CACTTTTGAT	CTATACATGA	AGGATATGCC	ACCATCTGCA	1440
GTA CTAGCA	TTCGTGTTTT	GTACGGAAAA	GTGAAATTAA	AAAGTGAAGA	ATTCTGAAGTT	1500
GGTTGGGTAA	ATATGTCCCT	AACCGATTGG	AGAGATGAAC	TACGACAAGG	ACAATTTTTTA	1560
TTCCATCTGT	GGGCTCCTGA	ACCGACTGCC	AATCGTAGTA	GGATCGGAGA	AAATGGAGCA	1620
AGGATAGGCA	CCAACGCAGC	GGTTACAATT	GAAATCTCAA	GTTATGGTGG	TAGAGTTCTGA	1680
ATGCCGAGTC	AAGGACAATA	CACATATCTC	GTCAAGCACC	GAAGTACTTG	GACGGAAACT	1740
TTGAATATTA	TGGGTGATGA	CTATGAGTCG	TGTATCAGAG	ATCCAGGATA	TAAGAAGCTT	1800
CAGATGCTTG	TCAAGAAGCA	TGAATCTGGA	ATTGTATTAG	AGGAAGATGA	ACAACGTCAT	1860
GTCTGGATGT	GGAGGAGATA	CATTCAAAG	CAGGAGCCTG	ATTTGCTCAT	TGTGCTCTCC	1920
GAAC TCGCAT	TTGTGTGGAC	TGATCGTGAG	AACTTTTCCG	AGCTCTATGT	GATGCTTGAA	1980
AAATGGAAAC	CGCCGAGTGT	GGCAGCCGCG	TTGACTTTGC	TTGGAAAACG	TTGCACGGAT	2040
CGTGTGATTC	GAAAGTTTGC	AGTGGAGAAG	TTGAATGAGC	AGCTGAGCCC	GGTCACATTC	2100

CATCTTTTCA	TATTGCCTCT	CATACAGGCG	TTGAAGTACG	AACCGCGTGC	TCAATCGGAA	2160
GTTGGAATGA	TGCTCTTGAC	TAGAGCTCTC	TGCGATTATC	GAATTGGACA	TCGACTTTTC	2220
TGGCTGCTCC	GTGCAGAGAT	TGCTCGTTTG	AGAGATTGTG	ATCTGAAAAG	TGAAGAATAT	2280
CGCCGTATCT	CACTTCTGAT	GGAAGCTTAC	CTCCGTGGAA	ATGAAGAGCA	CATCAAGATC	2340
ATCACCCGAC	AAGTTGACAT	GGTTGATGAG	CTCACACGAA	TCAGCACTCT	TGTCAAAGGA	2400
ATGCCAAAAG	ATGTTGCTAC	GATGAAACTG	CGTGACGAGC	TTCGATCGAT	TAGTCATAAA	2460
ATGGAAAATA	TGGATTCTCC	ACTGGATCCT	GTGTACAAAC	TGGGTGAAAT	GATAATCGAC	2520
AAAGCCATCG	TCCTAGGAAG	TGCAAAACGT	CCGTTAATGC	TTCACTGGAA	GAACAAAAT	2580
CCAAAGAGTG	ACCTGCACCT	TCCGTTCTGT	GCAATGATCT	TCAAGAATGG	AGACGATCTT	2640
CGCCAGGACA	TGCTTGTTCT	TCAAGTTCTC	GAAGTTATGG	ATAACATCTG	GAAGGCTGCA	2700
AACATTGATT	GCTGTTTGAA	CCCGTACGCA	GTTCTTCCAA	TGGGAGAAAT	GATTGGAATT	2760
ATTGAAGTTG	TGCCTAATTG	TAAAACAATA	TTCGAGATTC	AAGTTGGAAC	AGGATTCATG	2820
AATACAGCAG	TTCGGAGTAT	TGATCCTTCG	TTTATGAATA	AGTGGATTTCG	GAAACAATGC	2880
GGAATTGAAG	ATGAAAAGAA	GAAAAGCAAA	AAGGACTCTA	CGAAAAATCC	CATCGAAAAG	2940
AAGATTGATA	ATACTCAAGC	CATGAAGAAA	TATTTTGAAA	GTGTCGATCG	ATTCCTATAC	3000
TCGTGTGTTG	GATATTCAGT	TGCCACGTAC	ATAATGGGAA	TCAAGGATCG	TCACAGTGAT	3060
AATCTGATGC	TCACTGAAGA	TGGAAAATAT	GTCCACATTG	ATTTTCGGTCA	CATTTTGCGA	3120
CACGGAAAGA	CCAAACTTGG	GATCCAGCGA	GATCGTCAAC	CGTTTATTCT	AACCGAACAC	3180
TTTATGACAG	TGATTTCGATC	GGGTAAATCT	GTGGATGGAA	ATTCGCATGA	GCTACAAAAA	3240
TTCAAAACGT	TATGCGTCGA	AGCCTACGAA	GTAATGTGGA	ATAATCGAGA	TTTGTTTCGTT	3300
TCCTTGTTCA	CCTTGATGCT	CGGAATGGAG	TTGCCTGAGC	TGTCGACGAA	AGCGGATTTC	3360
GATCATTTGA	AGAAAACCCT	CTTCTGCAAT	GGAGAAAGCA	AAGAAGAAGC	GAGAAAGTTT	3420
TTCGCTGGAA	TCTACGAAGA	AGCCTTCAAT	GGATCATGGT	CTACCAAAC	GAATTGGCTC	3480
TTCCACGCAG	TCAAACACTA	CTGA				3504

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTGGTTCA TTTCCCAACC

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTAACTCAC CTAGTCTTCG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACAATTACA GGCCGATCC

19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGCCACGCA AGAAACTCAC

20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAAAGATGG AATGTGACCG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATCTGAAGCG TTCTTATATC

20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGCTCCATTT TCTCCGATCC

20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1068 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Pro	Pro	Arg	Pro	Ser	Ser	Gly	Glu	Leu	Trp	Gly	Ile	His	Leu	Met
1				5					10					15	
Pro	Pro	Arg	Ile	Leu	Val	Glu	Cys	Leu	Leu	Pro	Asn	Gly	Met	Ile	Val
			20					25					30		
Thr	Leu	Glu	Cys	Leu	Arg	Glu	Ala	Thr	Leu	Val	Thr	Ile	Lys	His	Glu
		35					40					45			
Leu	Phe	Arg	Glu	Ala	Arg	Lys	Tyr	Pro	Leu	His	Gln	Leu	Leu	Gln	Asp
	50				55				60						
Glu	Thr	Ser	Tyr	Ile	Phe	Val	Ser	Val	Thr	Gln	Glu	Ala	Glu	Arg	Glu
65				70					75					80	
Glu	Phe	Phe	Asp	Glu	Thr	Arg	Arg	Leu	Cys	Asp	Leu	Arg	Leu	Phe	Gln
			85					90					95		
Pro	Phe	Leu	Lys	Val	Ile	Glu	Pro	Val	Gly	Asn	Arg	Glu	Glu	Lys	Ile
		100					105					110			
Leu	Asn	Arg	Glu	Ile	Gly	Phe	Val	Ile	Gly	Met	Pro	Val	Cys	Glu	Phe
	115				120				125						
Asp	Met	Val	Lys	Asp	Pro	Glu	Val	Gln	Asp	Phe	Arg	Arg	Asn	Ile	Leu
	130				135				140						
Asn	Val	Cys	Lys	Glu	Ala	Val	Asp	Leu	Arg	Asp	Leu	Asn	Ser	Pro	His



145		150		155		160
Ser Arg Ala Met Tyr Val Tyr Pro Pro Asn Val Glu Ser Ser Pro Glu						
	165		170			175
Leu Pro Lys His Ile Tyr Asn Lys Leu Asp Lys Gly Gln Ile Ile Val						
	180		185			190
Val Ile Trp Val Ile Val Ser Pro Asn Asn Asp Lys Gln Lys Tyr Thr						
	195		200			205
Leu Lys Ile Asn His Asp Cys Val Pro Glu Gln Val Ile Ala Glu Ala						
	210		215			220
Ile Arg Lys Lys Thr Arg Ser Met Leu Leu Ser Ser Glu Gln Leu Lys						
225		230		235		240
Leu Cys Val Leu Glu Tyr Gln Gly Lys Tyr Ile Leu Lys Val Cys Gly						
	245		250			255
Cys Asp Glu Tyr Phe Leu Glu Lys Tyr Pro Leu Ser Gln Tyr Lys Tyr						
	260		265			270
Ile Arg Ser Cys Ile Met Leu Gly Arg Met Pro Asn Leu Met Leu Met						
	275		280			285
Ala Lys Glu Ser Leu Tyr Ser Gln Leu Pro Ile Asp Ser Phe Thr Met						
	290		295			300
Pro Ser Tyr Ser Arg Arg Ile Ser Thr Ala Thr Pro Tyr Met Asn Gly						
305		310		315		320
Glu Thr Ser Thr Lys Ser Leu Trp Val Ile Asn Ser Ala Leu Arg Ile						
	325		330			335
Lys Ile Leu Cys Ala Thr Tyr Val Asn Val Asn Ile Arg Asp Ile Asp						
	340		345			350
Lys Ile Tyr Val Arg Thr Gly Ile Tyr His Gly Gly Glu Pro Leu Cys						
	355		360			365
Asp Asn Val Asn Thr Gln Arg Val Pro Cys Ser Asn Pro Arg Trp Asn						
	370		375			380
Glu Trp Leu Asn Tyr Asp Ile Tyr Ile Pro Asp Leu Pro Arg Leu Ala						
385		390		395		400
Arg Leu Cys Leu Ser Ile Cys Ser Val Lys Gly Arg Lys Gly Ala Lys						
	405		410			415
Glu Glu His Cys Pro Leu Ala Trp Gly Asn Ile Asn Leu Phe Asp Tyr						
	420		425			430
Thr Asp Thr Leu Val Ser Gly Lys Met Ala Leu Asn Leu Trp Pro Val						
	435		440			445
Pro His Gly Leu Glu Asp Leu Leu Asn Pro Ile Gly Val Thr Gly Ser						
	450		455			460
Asn Pro Asn Lys Glu Thr Pro Cys Leu Glu Leu Glu Phe Asp Trp Phe						
465		470		475		480
Ser Ser Val Val Lys Phe Pro Asp Met Ser Val Ile Glu Glu His Ala						
	485		490			495
Asn Trp Ser Val Ser Arg Glu Ala Gly Phe Ser Tyr Ser His Thr Gly						
	500		505			510
Leu Ser Asn Arg Leu Ala Arg Asp Asn Glu Leu Arg Glu Asn Asp Lys						
	515		520			525
Glu Gln Leu Arg Ala Leu Cys Thr Arg Asp Pro Leu Ser Glu Ile Thr						
	530		535			540
Glu Gln Glu Lys Asp Phe Leu Trp Ser His Arg His Tyr Cys Val Thr						
545		550		555		560

Ile	Pro	Glu	Ile	Leu	Pro	Lys	Leu	Leu	Leu	Ser	Val	Lys	Trp	Asn	Ser		
				565					570						575		
Arg	Asp	Glu	Val	Ala	Gln	Met	Tyr	Cys	Leu	Val	Lys	Asp	Trp	Pro	Pro		
			580					585					590				
Ile	Lys	Pro	Glu	Gln	Ala	Met	Glu	Leu	Leu	Asp	Cys	Asn	Tyr	Pro	Asp		
		595					600					605					
Pro	Met	Val	Arg	Ser	Phe	Ala	Val	Arg	Cys	Leu	Glu	Lys	Tyr	Leu	Thr		
	610					615					620						
Asp	Asp	Lys	Leu	Ser	Gln	Tyr	Leu	Ile	Gln	Leu	Val	Gln	Val	Leu	Lys		
625					630				635						640		
Tyr	Glu	Gln	Tyr	Leu	Asp	Asn	Leu	Leu	Val	Arg	Phe	Leu	Leu	Lys	Lys		
			645						650					655			
Ala	Leu	Thr	Asn	Gln	Arg	Ile	Gly	His	Phe	Phe	Phe	Trp	His	Leu	Lys		
			660					665					670				
Ser	Glu	Met	His	Asn	Lys	Thr	Val	Ser	Gln	Arg	Phe	Gly	Leu	Leu	Leu		
		675					680					685					
Glu	Ser	Tyr	Cys	Arg	Ala	Cys	Gly	Met	Tyr	Leu	Lys	His	Leu	Asn	Arg		
	690					695					700						
Gln	Val	Glu	Ala	Met	Glu	Lys	Leu	Ile	Asn	Leu	Thr	Asp	Ile	Leu	Lys		
705					710				715						720		
Gln	Glu	Lys	Lys	Asp	Glu	Thr	Gln	Lys	Val	Gln	Met	Lys	Phe	Leu	Val		
			725						730					735			
Glu	Gln	Met	Arg	Gln	Pro	Asp	Phe	Met	Asp	Ala	Leu	Gln	Gly	Phe	Leu		
			740					745					750				
Ser	Pro	Leu	Asn	Pro	Ala	His	Gln	Leu	Gly	Asn	Leu	Arg	Leu	Glu	Glu		
		755					760					765					
Cys	Arg	Ile	Met	Ser	Ser	Ala	Lys	Arg	Pro	Leu	Trp	Leu	Asn	Trp	Glu		
	770					775					780						
Asn	Pro	Asp	Ile	Met	Ser	Glu	Leu	Leu	Phe	Gln	Asn	Asn	Glu	Ile	Ile		
785					790					795					800		
Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr	Leu	Gln	Ile		
			805					810						815			
Ile	Arg	Ile	Met	Glu	Asn	Ile	Trp	Gln	Asn	Gln	Gly	Leu	Asp	Leu	Arg		
		820						825					830				
Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ser	Ile	Gly	Asp	Cys	Val	Gly	Leu	Ile		
		835					840					845					
Glu	Val	Val	Arg	Asn	Ser	His	Thr	Ile	Met	Gln	Ile	Gln	Cys	Lys	Gly		
	850					855					860						
Gly	Leu	Lys	Gly	Ala	Leu	Gln	Phe	Asn	Ser	His	Thr	Leu	His	Gln	Trp		
865					870					875					880		
Leu	Lys	Asp	Lys	Asn	Lys	Gly	Glu	Ile	Tyr	Asp	Ala	Ala	Ile	Asp	Leu		
			885						890					895			
Phe	Thr	Arg	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Thr	Phe	Ile	Leu	Gly		
		900						905					910				
Ile	Gly	Asp	Arg	His	Asn	Ser	Asn	Ile	Met	Val	Lys	Asp	Asp	Gly	Gln		
	915						920					925					
Leu	Phe	His	Ile	Asp	Phe	Gly	His	Phe	Leu	Asp	His	Lys	Lys	Lys	Lys		
	930					935					940						
Phe	Gly	Tyr	Lys	Arg	Glu	Arg	Val	Pro	Phe	Val	Leu	Thr	Gln	Asp	Phe		
945					950					955					960		
Leu	Ile	Val	Ile	Ser	Lys	Gly	Ala	Gln	Glu	Tyr	Thr	Lys	Thr	Arg	Glu		

				965						970						975			
Phe	Glu	Arg	Phe	Gln	Glu	Met	Cys	Tyr	Lys	Ala	Tyr	Leu	Ala	Ile	Arg				
			980						985					990					
Gln	His	Ala	Asn	Leu	Phe	Ile	Asn	Leu	Phe	Ser	Met	Met	Leu	Gly	Ser				
		995					1000					1005							
Gly	Met	Pro	Glu	Leu	Gln	Ser	Phe	Asp	Asp	Ile	Ala	Tyr	Ile	Arg	Lys				
	1010					1015					1020								
Thr	Leu	Ala	Leu	Asp	Lys	Thr	Glu	Gln	Glu	Ala	Leu	Glu	Tyr	Phe	Thr				
025					1030					1035					1040				
Lys	Gln	Met	Asn	Asp	Ala	His	His	Gly	Gly	Trp	Thr	Thr	Lys	Met	Asp				
			1045						1050					1055					
Trp	Ile	Phe	His	Thr	Ile	Lys	Gln	His	Ala	Leu	Asn								
			1060						1065										

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Cys	Phe	Ser	Phe	Ile	Met	Pro	Pro	Ala	Met	Ala	Asp	Ile	Leu	Asp				
1				5					10					15					
Ile	Trp	Ala	Val	Asp	Ser	Gln	Ile	Ala	Ser	Asp	Gly	Ser	Ile	Pro	Val				
			20					25					30						
Asp	Phe	Leu	Leu	Pro	Thr	Gly	Ile	Tyr	Ile	Gln	Leu	Glu	Val	Pro	Arg				
		35				40					45								
Glu	Ala	Thr	Ile	Ser	Tyr	Ile	Lys	Gln	Met	Leu	Trp	Lys	Gln	Val	His				
	50					55				60									
Asn	Tyr	Pro	Met	Phe	Asn	Leu	Leu	Met	Asp	Ile	Asp	Ser	Tyr	Met	Phe				
65					70				75					80					
Ala	Cys	Val	Asn	Gln	Thr	Ala	Val	Tyr	Glu	Glu	Leu	Glu	Asp	Glu	Thr				
			85					90					95						
Arg	Arg	Leu	Cys	Asp	Val	Arg	Pro	Phe	Leu	Pro	Val	Leu	Lys	Leu	Val				
		100						105					110						
Thr	Arg	Ser	Cys	Asp	Pro	Gly	Glu	Lys	Leu	Asp	Ser	Lys	Ile	Gly	Val				
		115				120						125							
Leu	Ile	Gly	Lys	Gly	Leu	His	Glu	Phe	Asp	Ser	Leu	Lys	Asp	Pro	Glu				
	130					135					140								
Val	Asn	Glu	Phe	Arg	Arg	Lys	Met	Arg	Lys	Phe	Ser	Glu	Glu	Lys	Ile				
145				150					155					160					
Leu	Ser	Leu	Val	Gly	Leu	Ser	Trp	Met	Asp	Trp	Leu	Lys	Gln	Thr	Tyr				
			165					170					175						
Pro	Pro	Glu	His	Glu	Pro	Ser	Ile	Pro	Glu	Asn	Leu	Glu	Asp	Lys	Leu				
		180						185					190						
Tyr	Gly	Gly	Lys	Leu	Ile	Val	Ala	Val	His	Phe	Glu	Asn	Cys	Gln	Asp				



Leu	Leu	Asp	Phe	Asn	Tyr	Pro	Asp	Gln	Tyr	Val	Arg	Glu	Tyr	Ala	Val
610						615					620				
Gly	Cys	Leu	Arg	Gln	Met	Ser	Asp	Glu	Glu	Leu	Ser	Gln	Tyr	Leu	Leu
625					630					635					640
Gln	Leu	Val	Gln	Val	Leu	Lys	Tyr	Glu	Pro	Phe	Leu	Asp	Cys	Ala	Leu
				645					650					655	
Ser	Arg	Phe	Leu	Leu	Glu	Arg	Ala	Leu	Gly	Asn	Arg	Arg	Ile	Gly	Gln
			660					665					670		
Phe	Leu	Phe	Trp	His	Leu	Arg	Ser	Glu	Val	His	Ile	Pro	Ala	Val	Ser
		675					680					685			
Val	Gln	Phe	Gly	Val	Ile	Leu	Glu	Ala	Tyr	Cys	Arg	Gly	Ser	Val	Gly
	690					695					700				
His	Met	Lys	Val	Leu	Ser	Lys	Gln	Val	Glu	Ala	Leu	Asn	Lys	Leu	Lys
705					710					715					720
Thr	Leu	Asn	Ser	Leu	Ile	Lys	Leu	Asn	Ala	Val	Lys	Leu	Asn	Arg	Ala
				725					730					735	
Lys	Gly	Lys	Glu	Ala	Met	His	Thr	Cys	Leu	Lys	Gln	Ser	Ala	Tyr	Arg
			740					745					750		
Glu	Ala	Leu	Ser	Asp	Leu	Gln	Ser	Pro	Leu	Asn	Pro	Cys	Val	Ile	Leu
		755					760					765			
Ser	Glu	Leu	Tyr	Val	Glu	Lys	Cys	Lys	Tyr	Met	Asp	Ser	Lys	Met	Lys
	770					775					780				
Pro	Leu	Trp	Leu	Val	Tyr	Asn	Asn	Lys	Val	Phe	Gly	Glu	Asp	Ser	Val
785					790					795					800
Gly	Val	Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr
				805					810					815	
Leu	Gln	Met	Leu	Arg	Leu	Met	Asp	Leu	Leu	Trp	Lys	Glu	Ala	Gly	Leu
			820					825					830		
Asp	Leu	Arg	Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ala	Thr	Gly	Asp	Arg	Ser
		835					840					845			
Gly	Leu	Ile	Glu	Val	Val	Ser	Thr	Ser	Glu	Thr	Ile	Ala	Asp	Ile	Gln
	850					855					860				
Leu	Asn	Ser	Ser	Asn	Val	Ala	Ala	Ala	Ala	Ala	Phe	Asn	Lys	Asp	Ala
865					870					875					880
Leu	Leu	Asn	Trp	Leu	Lys	Glu	Tyr	Asn	Ser	Gly	Asp	Asp	Leu	Asp	Arg
				885					890					895	
Ala	Ile	Glu	Glu	Phe	Thr	Leu	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Ser
			900					905					910		
Tyr	Val	Leu	Gly	Ile	Gly	Asp	Arg	His	Ser	Asp	Asn	Ile	Met	Val	Lys
		915				920						925			
Lys	Thr	Gly	Gln	Leu	Phe	His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	Asn
	930					935					940				
Phe	Lys	Ser	Lys	Phe	Gly	Ile	Lys	Arg	Glu	Arg	Val	Pro	Phe	Ile	Leu
945					950					955					960
Thr	Tyr	Asp	Phe	Ile	His	Val	Ile	Gln	Gln	Gly	Lys	Thr	Gly	Asn	Thr
				965					970					975	
Glu	Lys	Phe	Gly	Arg	Phe	Arg	Gln	Cys	Glu	Asp	Ala	Tyr	Leu	Ile	
			980					985				990			
Leu	Arg	Arg	His	Gly	Asn	Leu	Phe	Ile	Thr	Leu	Phe	Ala	Leu	Met	Leu
		995				1000						1005			
Thr	Ala	Gly	Leu	Pro	Glu	Leu	Thr	Ser	Val	Lys	Asp	Ile	Gln	Tyr	Leu

1010	1015	1020
Lys Asp Ser Leu Ala Leu Gly Lys Ser Glu Glu Glu Ala Leu Lys Gln		
025	1030	1035
Phe Lys Gln Lys Phe Asp Glu Ala Leu Arg Glu Ser Trp Thr Thr Lys		1040
	1045	1050
Val Asn Trp Met Ala His Thr Val Arg Lys Asp Tyr Arg Ser		1055
	1060	1065
		1070

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Glu	Leu	Glu	Asn	Tyr	Lys	Gln	Pro	Val	Val	Leu	Arg	Glu	Asp	Asn
1				5				10						15	
Cys	Arg	Arg	Arg	Arg	Arg	Met	Lys	Pro	Arg	Ser	Ala	Ala	Ser	Leu	Ser
			20					25					30		
Ser	Met	Glu	Leu	Ile	Pro	Ile	Glu	Phe	Val	Leu	Pro	Thr	Ser	Gln	Arg
		35					40					45			
Lys	Cys	Lys	Ser	Pro	Glu	Thr	Ala	Leu	Leu	His	Val	Ala	Gly	His	Gly
	50					55				60					
Asn	Val	Glu	Gln	Met	Lys	Ala	Gln	Val	Trp	Leu	Arg	Ala	Leu	Glu	Thr
65				70					75					80	
Ser	Val	Ala	Ala	Asp	Phe	Tyr	His	Arg	Leu	Gly	Pro	His	His	Phe	Leu
			85					90					95		
Leu	Leu	Tyr	Gln	Lys	Lys	Gly	Gln	Trp	Tyr	Glu	Ile	Tyr	Asp	Lys	Tyr
		100					105					110			
Gln	Val	Val	Gln	Thr	Leu	Asp	Cys	Leu	Arg	Tyr	Trp	Lys	Ala	Thr	His
	115					120					125				
Arg	Ser	Pro	Gly	Gln	Ile	His	Leu	Val	Gln	Arg	His	Pro	Pro	Ser	Glu
	130				135				140						
Glu	Ser	Gln	Ala	Phe	Gln	Arg	Gln	Leu	Thr	Ala	Leu	Ile	Gly	Tyr	Asp
145				150				155						160	
Val	Thr	Asp	Val	Ser	Asn	Val	His	Asp	Asp	Glu	Leu	Glu	Phe	Thr	Arg
			165				170						175		
Arg	Gly	Leu	Val	Thr	Pro	Arg	Met	Ala	Glu	Val	Ala	Ser	Arg	Asp	Pro
	180					185						190			
Lys	Leu	Tyr	Ala	Met	His	Pro	Trp	Val	Thr	Ser	Lys	Pro	Leu	Pro	Glu
	195					200					205				
Tyr	Leu	Trp	Lys	Lys	Ile	Ala	Asn	Asn	Cys	Ile	Phe	Ile	Val	Ile	His
	210				215					220					
Arg	Ser	Thr	Thr	Ser	Gln	Thr	Ile	Lys	Val	Ser	Pro	Asp	Asp	Thr	Pro
225				230				235						240	
Gly	Ala	Ile	Leu	Gln	Ser	Phe	Phe	Thr	Lys	Met	Ala	Lys	Lys	Lys	Ser

				245					250				255				
Leu	Met	Asp	Ile	Pro	Glu	Ser	Gln	Ser	Glu	Gln	Asp	Phe	Val	Leu	Arg		
			260					265					270				
Val	Cys	Gly	Arg	Asp	Glu	Tyr	Leu	Val	Gly	Glu	Thr	Pro	Ile	Lys	Asn		
		275					280					285					
Phe	Gln	Trp	Val	Arg	His	Cys	Leu	Lys	Asn	Gly	Glu	Glu	Ile	His	Val		
		290				295					300						
Val	Leu	Asp	Thr	Pro	Pro	Asp	Pro	Ala	Leu	Asp	Glu	Val	Arg	Lys	Glu		
305					310					315					320		
Glu	Trp	Pro	Leu	Val	Asp	Asp	Cys	Thr	Gly	Val	Thr	Gly	Tyr	His	Glu		
			325						330					335			
Gln	Leu	Thr	Ile	His	Gly	Lys	Asp	His	Glu	Ser	Val	Phe	Thr	Val	Ser		
			340					345					350				
Leu	Trp	Asp	Cys	Asp	Arg	Lys	Phe	Arg	Val	Lys	Ile	Arg	Gly	Ile	Asp		
		355					360					365					
Ile	Pro	Val	Leu	Pro	Arg	Asn	Thr	Asp	Leu	Thr	Val	Phe	Val	Glu	Ala		
		370				375					380						
Asn	Ile	Gln	His	Gly	Gln	Gln	Val	Leu	Cys	Gln	Arg	Arg	Thr	Ser	Pro		
385					390					395					400		
Lys	Pro	Phe	Thr	Glu	Glu	Val	Leu	Trp	Asn	Val	Trp	Leu	Glu	Phe	Ser		
			405						410					415			
Ile	Lys	Ile	Lys	Asp	Leu	Pro	Lys	Gly	Ala	Leu	Leu	Asn	Leu	Gln	Ile		
			420					425					430				
Tyr	Cys	Gly	Lys	Ala	Pro	Ala	Leu	Ser	Ser	Lys	Ala	Ser	Ala	Glu	Ser		
		435					440				445						
Pro	Ser	Ser	Glu	Ser	Lys	Gly	Lys	Val	Arg	Leu	Leu	Tyr	Tyr	Val	Asn		
		450				455					460						
Leu	Leu	Leu	Ile	Asp	His	Arg	Phe	Leu	Leu	Arg	Arg	Gly	Glu	Tyr	Val		
465					470					475					480		
Leu	His	Met	Trp	Gln	Ile	Ser	Gly	Lys	Gly	Glu	Asp	Gln	Gly	Ser	Phe		
			485						490					495			
Asn	Ala	Asp	Lys	Leu	Thr	Ser	Ala	Thr	Asn	Pro	Asp	Lys	Glu	Asn	Ser		
			500					505					510				
Met	Ser	Ile	Ser	Ile	Leu	Leu	Asp	Asn	Tyr	Cys	His	Pro	Ile	Ala	Leu		
		515					520					525					
Pro	Lys	His	Gln	Pro	Thr	Pro	Asp	Pro	Glu	Gly	Asp	Arg	Val	Arg	Ala		
		530				535					540						
Glu	Met	Pro	Asn	Gln	Leu	Arg	Lys	Gln	Leu	Glu	Ala	Ile	Ile	Ala	Thr		
545					550					555					560		
Asp	Pro	Leu	Asn	Pro	Leu	Thr	Ala	Glu	Asp	Lys	Glu	Leu	Leu	Trp	His		
			565					570						575			
Phe	Arg	Tyr	Glu	Ser	Leu	Lys	His	Pro	Lys	Ala	Tyr	Pro	Lys	Leu	Phe		
			580					585					590				
Ser	Ser	Val	Lys	Trp	Gly	Gln	Gln	Glu	Ile	Val	Ala	Lys	Thr	Tyr	Gln		
		595					600					605					
Leu	Leu	Ala	Arg	Arg	Glu	Val	Trp	Asp	Gln	Ser	Ala	Leu	Asp	Val	Gly		
		610				615					620						
Leu	Thr	Met	Gln	Leu	Leu	Asp	Cys	Asn	Phe	Ser	Asp	Glu	Asn	Val	Arg		
625					630					635					640		
Ala	Ile	Ala	Val	Gln	Lys	Leu	Glu	Ser	Leu	Glu	Asp	Asp	Asp	Val	Leu		
			645					650						655			

His	Tyr	Leu	Leu	Gln	Leu	Val	Gln	Ala	Val	Lys	Phe	Glu	Pro	Tyr	His	
		660						665					670			
Asp	Ser	Ala	Leu	Ala	Arg	Phe	Leu	Leu	Lys	Arg	Gly	Leu	Arg	Asn	Lys	
		675					680					685				
Arg	Ile	Gly	His	Phe	Leu	Phe	Trp	Phe	Leu	Arg	Ser	Glu	Ile	Ala	Gln	
	690					695					700					
Ser	Arg	His	Tyr	Gln	Gln	Arg	Phe	Ala	Val	Ile	Leu	Glu	Ala	Tyr	Leu	
705					710					715					720	
Arg	Gly	Cys	Gly	Thr	Ala	Met	Leu	His	Asp	Phe	Thr	Gln	Gln	Val	Gln	
				725					730					735		
Val	Ile	Glu	Met	Leu	Gln	Lys	Val	Thr	Leu	Asp	Ile	Lys	Ser	Leu	Ser	
			740					745					750			
Ala	Glu	Lys	Tyr	Asp	Val	Ser	Ser	Gln	Val	Ile	Ser	Gln	Leu	Lys	Gln	
		755					760					765				
Lys	Leu	Glu	Asn	Leu	Gln	Asn	Ser	Gln	Leu	Pro	Glu	Ser	Phe	Arg	Val	
	770					775					780					
Pro	Tyr	Asp	Pro	Gly	Leu	Lys	Ala	Gly	Ala	Leu	Ala	Ile	Glu	Lys	Cys	
785					790					795					800	
Lys	Val	Met	Ala	Ser	Lys	Lys	Lys	Pro	Leu	Trp	Leu	Glu	Phe	Lys	Cys	
			805						810					815		
Ala	Asp	Pro	Thr	Ala	Leu	Ser	Asn	Glu	Thr	Ile	Gly	Ile	Ile	Phe	Lys	
			820					825					830			
His	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Ile	Leu	Gln	Ile	Leu	Arg	
		835					840					845				
Ile	Met	Glu	Ser	Ile	Trp	Glu	Thr	Glu	Ser	Leu	Asp	Leu	Cys	Leu	Leu	
	850					855					860					
Pro	Tyr	Gly	Cys	Ile	Ser	Thr	Gly	Asp	Lys	Ile	Gly	Met	Ile	Glu	Ile	
865					870					875					880	
Val	Lys	Asp	Ala	Thr	Thr	Ile	Ala	Lys	Ile	Gln	Gln	Ser	Thr	Val	Gly	
			885						890					895		
Asn	Thr	Gly	Ala	Phe	Lys	Asp	Glu	Val	Leu	Asn	His	Trp	Leu	Lys	Glu	
		900						905					910			
Lys	Ser	Pro	Thr	Glu	Glu	Lys	Phe	Gln	Ala	Ala	Val	Glu	Arg	Phe	Val	
		915					920					925				
Tyr	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Thr	Phe	Val	Leu	Gly	Ile	Gly	
	930					935					940					
Asp	Arg	His	Asn	Asp	Asn	Ile	Met	Ile	Thr	Glu	Thr	Gly	Asn	Leu	Phe	
945					950					955					960	
His	Ile	Asp	Phe	Gly	His	Ile	Leu	Gly	Asn	Tyr	Lys	Ser	Phe	Leu	Gly	
			965						970					975		
Ile	Asn	Lys	Glu	Arg	Val	Pro	Phe	Val	Leu	Thr	Pro	Asp	Phe	Leu	Phe	
		980						985					990			
Val	Met	Gly	Thr	Ser	Gly	Lys	Lys	Thr	Ser	Pro	His	Phe	Gln	Lys	Phe	
		995					1000					1005				
Gln	Asp	Ile	Cys	Val	Lys	Ala	Tyr	Leu	Ala	Leu	Arg	His	His	Thr	Asn	
	1010					1015					1020					
Leu	Leu	Ile	Ile	Leu	Phe	Ser	Met	Met	Leu	Met	Thr	Gly	Met	Pro	Gln	
025					1030					1035					1040	
Leu	Thr	Ser	Lys	Glu	Asp	Ile	Glu	Tyr	Ile	Arg	Asp	Ala	Leu	Thr	Val	
			1045						1050				1055			
Gly	Lys	Asn	Glu	Glu	Asp	Ala	Lys	Lys	Tyr	Phe	Leu	Asp	Gln	Ile	Glu	



	1060		1065		1070
Val	Cys	Arg	Asp	Lys	Gly
				Trp	Thr
				Val	Gln
				Phe	Asn
				Trp	Phe
				Leu	His
	1075		1080		1085
Leu	Val	Leu	Gly	Ile	Lys
				Gln	Gly
				Glu	Lys
				His	Ser
				Ala	
	1090		1095		1100

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile	Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu
1				5								10

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His	Ile	Asp	Phe	Gly	His
1				5	